

1 MEA---EQRRAAGASEGATPCLEAVPEVAPBPAT-----hHac3.pro
 1 -----hHac2.pro
 1 MDARGGGRGREGSPGATPA[PC]PPPP[PE]AP[PE]GGPGAPPQHPRAEALPPEAADEGGPRGRhHac1.pro
 32 -----AASGP-----hHac3.pro
 1 -----hHac2.pro
 61 LRSRDSSCGRPGTPGAASTAKGSPNGECGRGEPCQSPAGPEGARGPKVSFSCRGAAASGP-----hHac1.pro
 37 I[PKS]GP-----[EEK]-----RRH[GT]LLO[BT]VNKFSLRV[FGS]HKAVERI[EQE]hHac3.pro
 1 -----K[EQE]-----hHac2.pro
 121 A[PGP]GAEEAGSEAGPAGE[PE]RGSQASFMRQ[FGA]LLO[BT]GVNKFSLRM[FGS]OKAVERI[EQE]hHac1.pro
 77 RVKSAGAWI[HPY]SDREFYWDLIML[IT]MVGNI[LV]LPVGITFFKEENSPWIVENV[LS]DTFhHac3.pro
 5 RVKTAGFWI[HPY]SDREFYWDLIMLIMVGNI[LV]IPVGITFF[EQ]TT[PWI]ENVASDTVhHac2.pro
 181 RVKSAGAWI[HPY]SDREFYWDFTMLL[FMV]GNLIIPVGITFFKDETTA[PWI]ENVV[LS]DTFhHac1.pro
 137 FLDDLVLNFGTGVMEGA[E]LLA[BR]ATRTR[KL]RTWELV[DL]ISSIPVDYIFL[V]ELEPRLhHac3.pro
 65 FLDDLIMNFGTGVNE[DS]EII[LD]BKVLK[MYL]KSWFVVD[FI]SSIPVDYIFLIVEKG--MhHac2.pro
 241 FLDDLVLNFGTGVIE[DN]TEI[LD]PEKIKK[KL]YLRTWFWVD[FM]SSIPVDYIFLIVEKG--IhHac1.pro
 197 DAEVYKTARALRIVRFTKILSLRLRLSLRIRYIHWEEIFHMTYDLASAVVRIFNLIGHHac3.pro
 123 DSEVYKTARALRIVRFTKILSLRLRLSLRIRYIHWEEIFHMTYDLASAVVRIFNLIGHHac2.pro
 299 DSEVYKTARALRIVRFTKILSLRLRLSLRIRYIHWEEIFHMTYDLASAVMR[IC]NLIShHac1.pro
 257 MMLLLCHWDFCLQFLVPM[LD]FPDPCWVSINHMVNHSWGRQYSHALFKAMSHMLCIGYQhHac3.pro
 183 MMLLLCHWDFCLQFLVPL[LD]FPDPCWVSINEMVN[DSW]GKQYSYALFKAMSHMLCIGYGAhHac2.pro
 359 MMLLLCHWDFCLQFLVPM[LD]FPDPCWVSINGMVNHSWSELYSFFALFKAMSHMLCIGYGRhHac1.pro
 317 QAPVGMHDMWLTMLSMIVGATCYAMFIGHATALIQ[LD]SSRRQYQEKYKQVEQYMSFHKLhHac3.pro
 243 QAPVSM[DI]WLTMLSMIVGATCYAMFVGHATALIQ[LD]SSRRQYQEKYKQVEQYMSFHKLhHac2.pro
 419 QAPFSMTIDTWLTMLSMIVGATCYAMFIGHATALIQ[LD]SSRRQYQEKYKQVEQYMSFHKLhHac1.pro

377 PADTRQRIHEYYEHRYQGKMFDEESILGEISEPLREEIINFICRGLVAHMPFLFAHADPSPF hHac3.pro
303 PADMRQKIHDYEHRYQGKI FDEENILNELNDPLREEIVNFNCRKLVATMPLFANADPNF hHac2.pro
479 PADFRQKIHDYEHRYQGKMEDEDSILGELNGPLREEIVNFNCRKLVASMPLEFANADPNF hHac1.pro

437 VTAMLTKLRFEFVQPGDLVVREGSVGRKMYFIZHGLLSVLARGARDTRLTGDSYFGEICL hHac3.pro
363 VTAMLSKLRFEFVQPGDYIIREGAVGKKMYFIZHGVAGVITKSSKEMKLTGDSYFGEICL hHac2.pro
539 VTAMLTKLKFEFVQPGDYIIREGTIGKKMYFIZHGVSVLTGKEMKLSGDSYFGEICL hHac1.pro

497 LTRGRRTASVRADTYCRLYSLSVDHFNALVEEFPMMRRAFETVAMDRLIRIGKKNISILQR hHac3.pro
423 LTKGRRTASVRADTYCRLYSLSVDNFNEVLEEYPMRRAFETVAIDRLDRIGKKNISILIQ hHac2.pro
599 LTRGRRTASVRADTYCRLYSLSVDNFNEVLEEYPMRRAFETVAIDRLDRIGKKNISILIH hHac1.pro

557 R-RSEPSPG---SSGGIMEQHIVQHDRDMARGVRGRAPSTGAQISGKPVLEFVLVHAPIQ hHac3.pro
483 KFKDLNTGVFNNOENELKQIVKHDREMVQAIAPIYPMQMTILNSTSTTPTSRMRTQ hHac2.pro
459 KVQHDLSGVFNNOENALIQELVKYDREMVQQA---ELQVRVGL----- hHac1.pro

613 AAATSNVAIALTHORGPIPLSP-DSPATLIARSANRSAGSPA---SPLVPVR---AGPW hHac3.pro
543 SPPVYTATSLSHSNLHSPSPSTQTPQPSAILSPCSYTTAMCSFPVQSPIAARTFHYASPT hHac2.pro
700 -----FPPPEPPQVTSATLQQA-AMSFQ-PQVAPLVGP-LALGSPR hHac1.pro

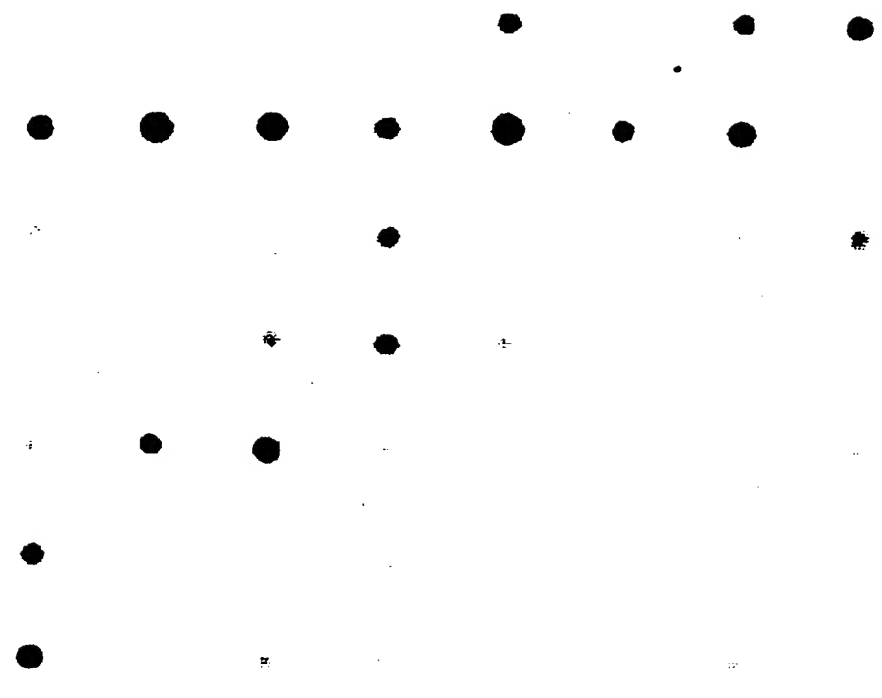
666 ASTSRLFAE-PARTLHASLSRAGRSQVSLGPPPGGG-----GRRIGPR hHac3.pro
603 ASQLSIMQQPQQVQQSQPPQRQPPQF-SPPQPTPGSSTPKNEVHKSTQALHNTNLTRE hHac2.pro
743 LVRRPPGEPAPAAASPGPFPASPPGAPASPRAPRTSPYGGPLAAPLAGPALPARRLSRA hHac1.pro

709 GRPLSASQPSLPQRAICDGSPGRKSGS-ERI-----PPSGILAKPPRTAQPP-- hHac3.pro
662 VRPESAMQPSLPHEVS--TLISRHPTVGESIASIPQPVTAVPGTGLQAGGRSTVPQRVT hHac2.pro
803 SRPLSASQPSLPHGAPGPAASTREASSSTPRIGPTAARAAPSPDRRDSASPGAAGGL- hHac1.pro

756 --RPPVPEPATPRGLQLSANM. hHac3.pro
720 FFRQMSSGAIPENRGVLPAPLPLITPHPKK hHac2.pro
862 -----DQDSARSRLSNL. hHac1.pro



FIG. 2A.



whole brain	amygdala	caudate nucleus	cerebellum	cerebral cortex	frontal lobe	hippocampus	medulla oblongata
occipital lobe	putamen	substantia nigra	temporal lobe	thalamus	nucleus accumbens	spinal cord	
heart	aorta	skeletal muscle	colon	bladder	uterus	prostate	stomach
testis	ovary	pancreas	pituitary gland	adrenal gland	thyroid gland	salivary gland	mammary gland
kidney	liver	small intestine	spleen	thymus	peripheral leukocyte	lymph node	bone marrow
appendix	lung	trachea	placenta				
fetal brain	fetal heart	fetal kidney	fetal liver	fetal spleen	fetal thymus	fetal lung	

FIG. 2B.

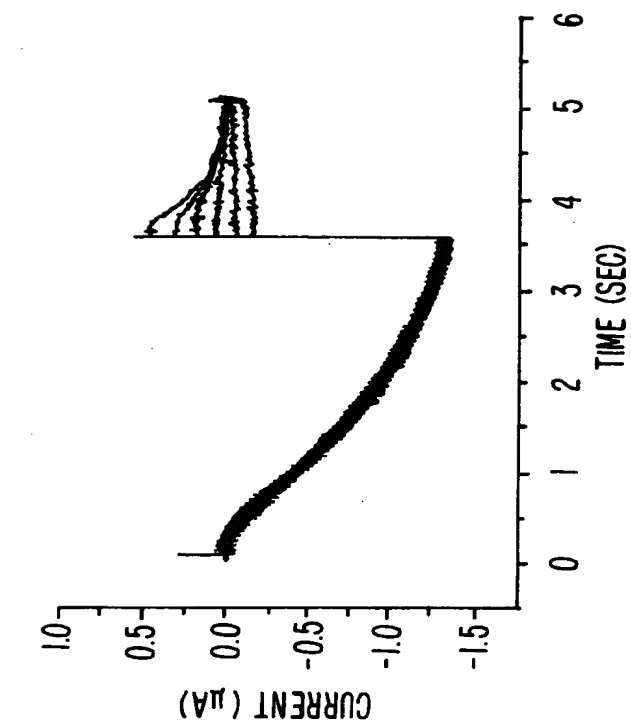


FIG. 3B.

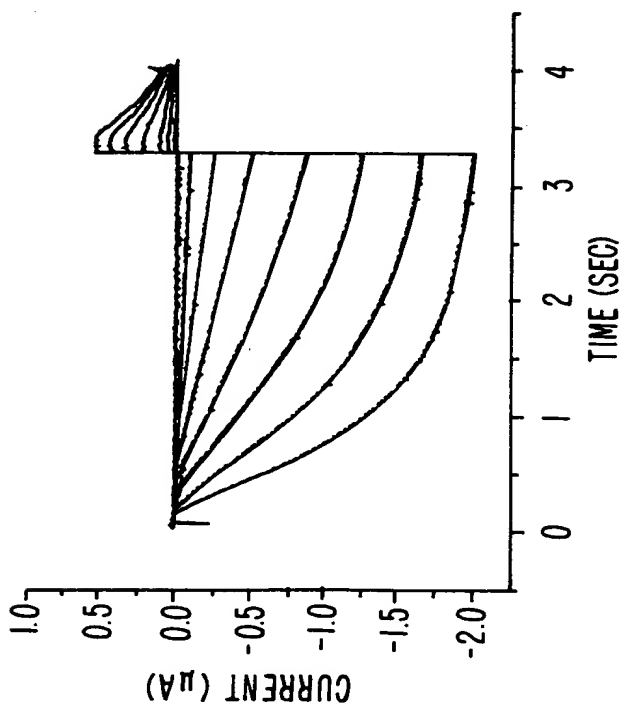


FIG. 3A.

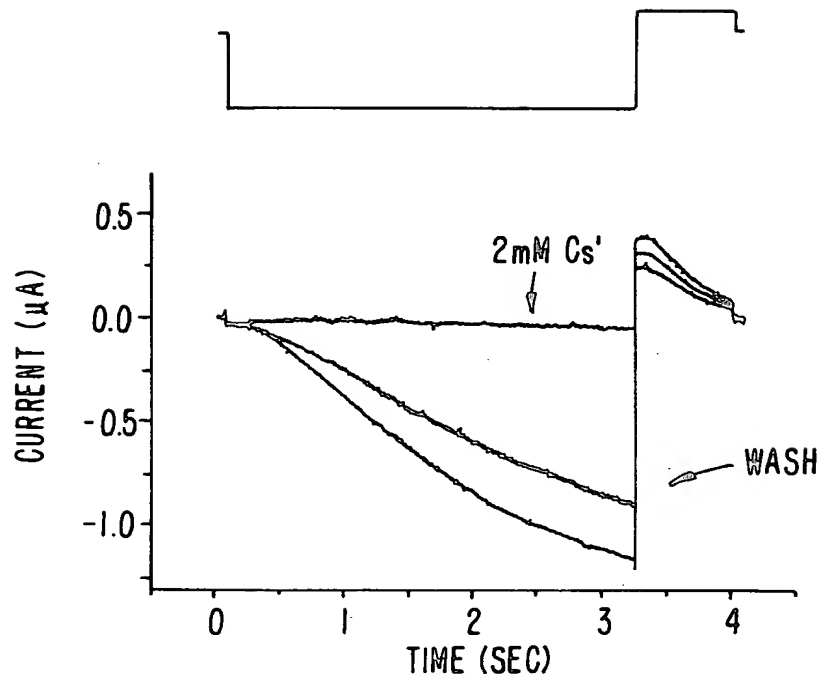


FIG. 4.